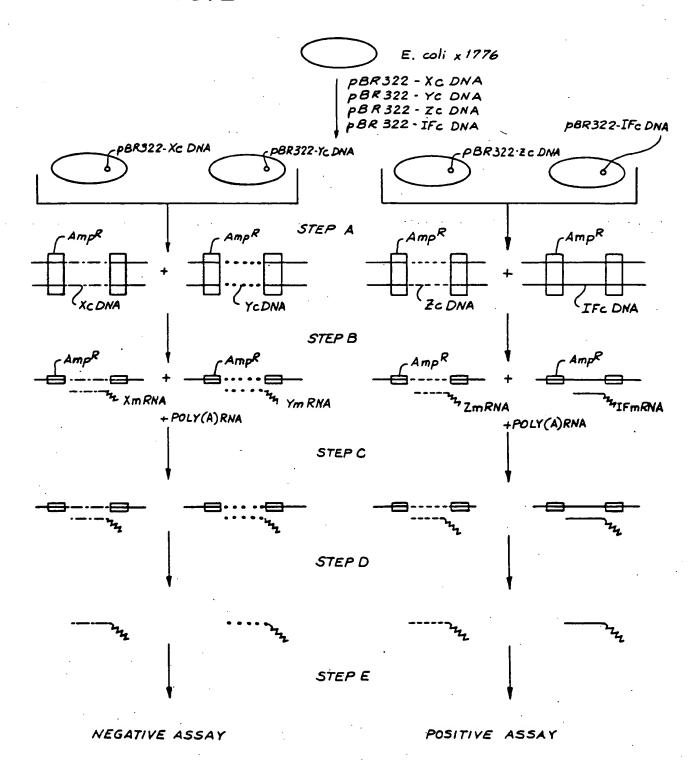


FIG. 2



F1G.3

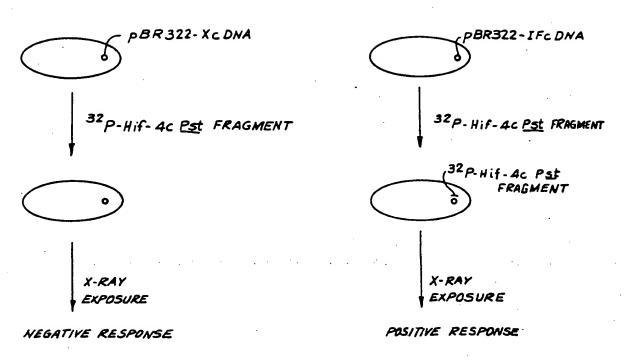
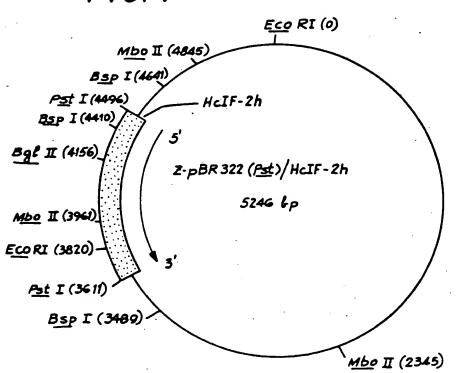
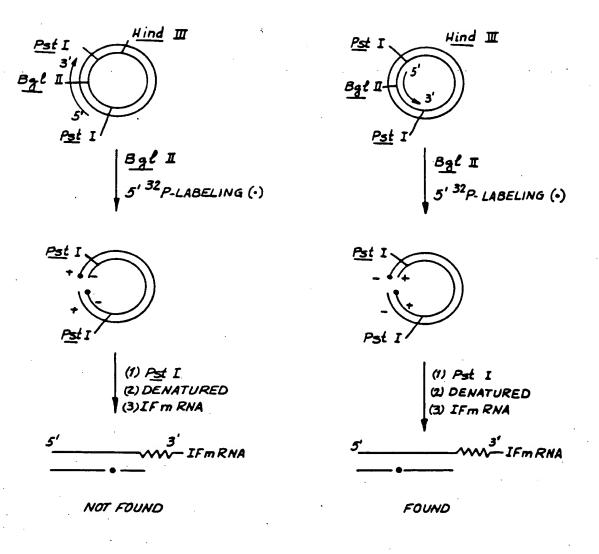


FIG. 4



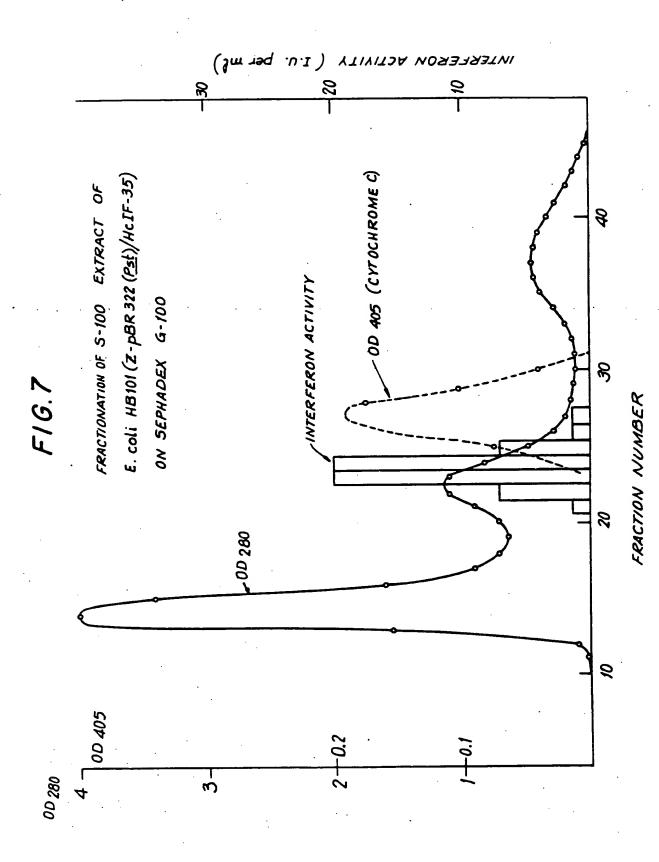


MetserIleGloHisPheArgvalAlaLeuIleProPhePheAlaAlaPheCysLeuProValPheAlaHisProLeuGloGlo MetSerIleGlnH1sPheArgValAlaLeuIleProPhePheAlaAlaPheCysLeuProValPheAlaH1sArgCysSerAsn ATGAGTATTCAACATTTCCGTGTCGCCCTTATTCCCTTTTTTGCGGCATTTTGCCTTCCTGTTTTTGCTCACCGCTGCAGGATG··· ATGAGTATTCAACATTTCCGTGTCGCCCTTATTCCCTTTTTTGCGGCATTTTGCCTTCCTGTTTTTGCTCACCCAGAACG MetSerijeGinHisPheArgValAlaLeuijeProPhePheAlaAlaPheCysLeuProValPheAlaHisProGluThr Pat CTGGTG...CCTGCAGCAATG... ProAlaAlaHet Pat 29 Leuval PKT279 PBR322

MetSerIleGlnHisPheArgvelAleLeulleProPhePheAleAleTITTGCGCATTTTGCCTTCCTGTTTTTGCTGAAACG pKT287

Alealealemet GCTGCAGCAATG···

Pst



S10 80 LEUMETVALLEU CTGATGGTCCTG ECOR11 Aval1	170 LEUMETLEULEU TTGATGCTCCTG SFANI ECORII	260 GLYASNGLNPHE GGCAACCAGTTC
S1 S10 S10 S1 B0 B0 METALASERPROPHEALALEULEUMETVALLEU B23CTCTAGGAGTCACCCAGAAGTATCTGCAATATCTACGATGGCCTCGCCCTTTGCTTTACTGATGGTCCTG ECOR BSP I ECOR	S20 1 VALVALLEUSERCYSLYSSERSERCYSSERLEUGLYCYSASPLEUPROGLUTHRHISSERLEUASPASNARGARGTHRLEUMETLEULEU GTGGTGCTCAGCTGCAAGTCAAGCTGCTCTCTGGGCTGTGATCTCCCTGAGACCCACAGCCCTGGATAACAGGAGGACCTTGATGCTCCTGAAACAGGAGGACCTTGATGCTCCTAGAAACAGGAGGACCTTGATGCTCCTAGAAAAAAAA	20 80 190 200 210 220 240 250 260 ALAGLNMETSERARGILESERPROSERSERCYSLEUMETASPARGHISASPPHEGLYPHEPROGLNGLUGLUPHEASPGLYASNGLNPHE GCACAAATGAGCAGAATCTCCTCCTCCTGTCTGATGGACAGACA
S1 60 METALASE GATGGCCTC BSP I	11 SSERLEUASI CAGCCTGGA ECORII	40 240 YPHEPROGLNG ATTTCCCCAGG
50 IGCAATATCTAC	130 ASPLEUPROGLUTHRHI GATCTCCCTGAGACCCA MBOI DDEI ECOPI	230 SHISASPPHEGL (CATGACTTTGG
40 4GAAGTATC1	1 130 YCYSASPLEU TIGTGATCTO MBOI	220 220 JMETASPARG SATGGACAGA
30 YGCAAGCCC/) 120 SSERLEUGL) CTCTCTGGG	30 210 RSERCYSLEU
20 ACCCATCTC/	S20 110 SSERSERCYS: GTCAAGCTGC ALUI	.200 ESERPROSEI CJCTCCTTC(
10 SGTTCAGAGTC, HINF	90 VALVALLEUSERCYSLY3 GTGGTGCTCAGCTGCAA0 DDE I PVUII	190 METSERARGILE: ATGAGCAGAATC
1 6 ₂₃ CTCTA(90 VALVALL GTGGTGG	20 180 ALAGLNM GCACAAA

FIG. 8

50 70 340 350 350 350 350 350 350 350 CAGAAGGCTCCAGCAGCCATCTCCATCAGCTGCTGCTGCAGCAGATCTTCACCACAAAGATTCATCTGCTGCTTGGATTCTTGCTTG	80 60 370 380 400 410 420 440 GLUASPLEULEUASPLYSPHECYSTHRGLULEUTYRGLNGLNEUASNASPLEUGLUALACYSVALMETGLNGLUGLUARGVALGLYGLU GAGGACCTCCTAGACAAATTCTGCACCGAACTCTACCAGCAGCTGAATGACTTGGAAGCCTGTGTGCAGGAGGGGGGGG	110 50 460 470 480 490 510 520 530 THRPROLEUMETASNALAASPSERILELEUALAVALLYSLYSTYRPHEARGARGILETHRLEUTYRLEUTHRGLULYSLYSTYRSERPRO ACTCCCTGATGAATGCGGACTCCATCTTGGCTGTGAAGAATACTTCCGAAGAATCACTCTCTATCTGACAGAAAAAAAA
340 RLYSASPSER AAAGATTCA HINF	O 430 LMETGLNGLU GATGCAGGAGI SFANI	520 RLEUTHRGLU TCTGACAGG
70 330 SUPHETHRTHF CCTTTACCACA	100 420 -UALACYSVALI AAGCCTGTGG	130 ⁵¹⁰ LETHRLEUTYRI TCACTCTCTATI
320 LNILEPHEASNLE AGATCTTCAACCT BGLII MBOI MBOII	410 SNASPLEUGI ATGACTTGG/	500 HEARGARGIL TTCCGAAGAAT MBOII
60 310 EUILEGLNGLNI TGATCCAGCAGA MBOI / BGL ECOP15 MBO	90 400 TYRGLNGLNLEUA TACCAGCAGCTGA ECOP15 PVUJI ALUI	0 490 LLYSLYSTYRF GAAGAAATAC] MBOII
60 300 3HISGLULEUILEG CCATGAGCTGATCC ALUMBOI ECOPIE	390 RGLULEUTYR CGAACTCTAC	120 480 ELEUALAVALI CTTGGCTGTG
290 ESERVALLEI FCTCTGTCCT	зво YSPHECYSTH AATTCTGCAC	470 LAASPSERIL CGGACTCCAT HINF
280 NLAPROALATU SCTCCAGCCAT	370 LEULEUASPLY ÇTCCTAGACAV I	460 LEUMETASNA CTGATGAATG
50 270 GLNLYSA CAGAAGG	80 360 GLUASPL GAGGACC AVAII	110 450 THRPROI ACTCCC

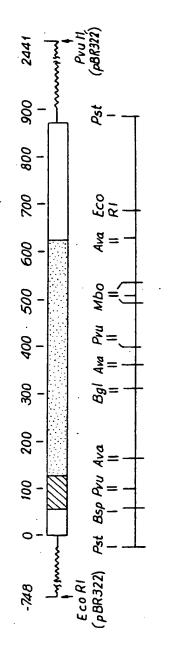
FIG. 9

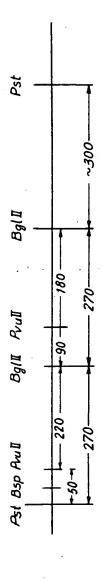
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166	620	ARGLYSGLU	TGTCAGAGCAGAAATCATGAGATCCCTCTCTTTATCAACAAACTTGCAAGAAGATTAAGGAGGAGGAATAACAT		
	61 0	ARGLEUARG	AGATTAAGG		
160	009	LVALARGALAGLUILEMETARGSERLEUSERLEUSERTHRASNLEUGLNGLUARGLEUARGARGLYSGLU	ACTTGCAAGAA		
	590	LEUSERTHRAS	TTATCAACAA		
	280	SERLEUSERI	NICCCTCTCT.	MaoI	
150	570	UILEMETARG	AATCATGAGA	₩.	
	260	/ALARGALAGI	STCAGAGCAG/		
_	550	CYSALATRPGLUVALN	GTGCCTGGGAGGTTG	EcoRII	
140	540	CYSALA	1676	_ 	

	6CTA		ACGT
710	GACTCTCACCCCT HINF HPH	800	TTGTTCATATA
700	ITTCAAAGA H1	790	VAATTATT
069	TGGTCCAACATGAAAACAATTCTTATTGACTCATACACCAGGTCACGCTTTCATGAATTCTGTCATTTCAAAGACTCTCACCCCTGCTA Avali Ecori Hinf Hph	780	TAACTATGACCATGCTGATAAACTGATTTATCTATTTAAATATTTTAACTATTCATAAGATTTAAATTATTTTGTTCATAACGT
089	ACGCTTTCA	770	ATTTAACTA'
019	ACACCAGGTC/ EcoR11	760	TTAAATATTT/
099	ATTGACTCAT Hinf	750	ATTTATCTAT
650	ACAATTCTT	740	GATAAACTE
640	ÇAACATGAAA I	730	TGACCATGCT
630	CTGGTCC Avall	720	TAACTA

CATGTGCACCTTTACACTGTGGTTAGTGTAATAAAACATGTTCCTTATATTTACTCAAAAAAC₁₅ 860 865 850 840 830 810 820 AccI

F1G. 10





Hif-II-206 ~ 850 bp.

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206(11)	6 _{1.3.} TTACTGGCCCCTC 1eu 1eu val ala 1eu -20	icccTc la leu
2н(1)	met ala ser pro phe ala leu lœu met val leu G23CTCTAGGTTCAGCAGAGCCAGAAGTATCTGCAATATCTACGATGCCCTCGCCTTTGCTTTACTGATGGTCCTG.	al leu ITCCTG. 1
206(11)	-30 -20 -10 10 20 30 40 50 50 CTGGGGGTGTGGGTCTCAAACCCACAGGGGGGGGGGGGG	so TÇCTĞ EU LEU
	-10 -10 10	
2H(I)	val val lou ser cys lys ser ser cys ser leu gly CYS ASP LEU PRO QLU THR HES SER LEU ASP ASN ARG ARG THR LEU MET LEU LEU. GTGGTGCTCAGCTGCAAGTCAAGCTGCTCTCTGGGCTGTGATCTCCCTGAGACCCACAGCCTGGATAACAGGAGGACCTTGATGCTCCTG. -30 -20 -20 -10 1 10 50	JEU LBU TCCTG. So

206(11)	60 70 80 140 140 120 140 140 140 140 140 140 140 140 140 14
2н(І)	ALA GLA PEL SER ARG ILE SER PRO SER SER CYS LEU MET ASP ARG HIS ASP FRE GLY PRO CLA CLU CLU CLU PRE ASP CLY ASA CLA PRE GCACAÇAATGAGGAGATCICCTICCTICCTCTGTGGAGAGAGATGGAGATTTGGATTTCCCCCAGGAGTTTGATGGCAACCAGTTC 60 120 130 140
:	
206(11)	O 160 170 GAAACÇATÇCCTGTÇCTÇCATGAGATGA GLU THR ILE PRO VAL LEU HIS GLU NET 1
2н(І)	50 50 GLN LYS ALA PRO ALA ILE SER VAL LEU IUS GLU LEU ILE GLN GLN ILE PIŒ ASN LEU PIŒ THR TUR LYS ASP SER SER ALA ALA TRP ASP CAGAAGGCTCCAGCCATCTCTGTCCTCCATGAGCTGATCCAGCAGATCTTGAACCTTTTACCACAAAAGATTCATCTGCTTGGGAT 150 160 160 210 220 230

FIG. 13

206(11)	240 250 260 370 280 290 300 320 320 520 300 310 320 5AGACCCTCTAGACAAATTCTACACTGAACTCTAGACTGAAAGACTCTAGACTGAAATTCTACACACTGAACTCTAGACTGAAATTCTACAAATTCTACACACAGACTGAAATTCTACAAATTCTACAAATTCTACAAATTCTACAAATTCTACAAATTCTACAAATTCTACAAATTCTACAAATTCTACAAATTCTACAAATTCTACAAATTCTACAAATTCTACAAATTCTACAAATTCTACAAATTCTACAAATTCTACAAATTACAAATTCTACAAATTCTACAAATTCTACAAATTCTACAAATTCTACAAAATTCTACAAAATTACAAAATTCTACAAAATTCTACAAAATTCTACAAAATTCTACAAAATTCTACAAAAAA	250 ACAAATTCTA SP LYS PHE TY	260 ACACTGÁACTCI R THR GLU LEU T	270 ACCAGCAGCTO YR GN GN LEU	280 SAATGACÇTGG ASN ASP LEU O	290 AAĞCÇTGTGT LU ALA CYS VAL	300 SATACAGGGG ILE GIN GLY	310 GTGGGGTGAC VAL GLY VAL TH	320 AGAG R GLU
2н(I)	80 GUI ASP LEU LEU ASP LYS THE CYS THR GLU LEU TYR GLY GLY LEU GLY GLU ASP LEU GLY GLY GLU ASP LEU LEU ASP LYS THE CYS THR GLY LEU ASP LEU LEU ASP LYS THE CYS THE CYS THR GLY LEU CASP CASP LEU GLY	SP LYS PHE CY AÇAAAİTCŢ (2 S 0	S THR CLU LEU T SCACCGAACTCT 260	90 YR GJN GJN LEU ACCAGCAGCTE 270	ASN ASP LEU C SAATGACTTGG 280 2	100 LU ALA CYS VAL AAGCCTGTGTG 90 30	MET GIN GIU (aw arg val Gi GAGAGGGTGGG io si	r cw AGAA, O
709(11)	330 340 350 370 360 410 ACTCCCCTGATGAAGGAGGACTCCATTCTGGCTGTGAGGAATACTTCCAAAGATCACTCTCTATCTGAAAGAAGAAGAAGAAGAGAAGCCCT TAR PRO LEU MET LYS GLU ASP SER ILE IEU ALA VAL ARG LYS TYR PRE GLN ARG ILE THR LEU TYR LEU LYS GLU LYS LYS TYR SER PRO	340 AGGAGGACTC IS ŒU ASP SE	SSO CATTCTGGCTG R ILE IEU ALA V	360 1GAGGAAATAC AL ARG LYS TYR 120	370 TTÇCAQAGA	380 TÇAČŢCTÇTA' LE THR LEU TYR	390 [CTGAAAGAG LEU LYS GUD 130	400 AAGÅAAJAÇA(LYS LYS TYR SE	410 1,cccT 8 Pro
2н(1)	THR PRO LEU MET ASN ALA ASP SER ILE LEU ALA VAL LYS LYS TYR PHE ARG ARG ILE THR LEU TYR LEU THR GLU LYS LYS TYR SER PRO ACTCCCCTGATGATGCGGACTCCATCTTGGCTGTGAAGAAATACTTCCGAAGAATCACTCTCTATCTGACAGAGAAGAAATACACTCT 330 340 450 410	N ALA ASP SE ATGCGGAÇTC 340	R ILE LEU ALA V CATCTTGGCTG 350	120 VAL LYS LYS TYR GTGAAGAAATAC 360	PE ARG ARG 1 TTCCGAAGA	LE THR LEU TYR I TÇACTCTCTATI	LEU THR CLU ICTGACAGAG	LYS LYS TYR SE AAGAAAJAÇA(jo	א אינ הקרכך 10

F1G.14

	420	430	440	450	094	470	480	490	005
206(11)	JGTGCCTGGGAGGTTGTCAGAGCAGAAATCATGAGATCTTTTGTCAAAACTTGCAAAAGTTGAAAGATTAAGAAGTAAGGAATGAAAA. CYS AIN TIP GIU VAL VAL ARG AIA GIU ILE MET ARG SIR PHE SIR LIU SIR THR ASN LIU GIN CIU SER LIU ARG SIR LYS CIU 140	GTÇÅGAĞCAĞI VAL ARG ALA GI	GTÇAGAGCAGAAATÇATGAGATÇITTTTÇTTTĞİCAACAAACITGCAAGAAGTTTAAGAAGTAAGGAA VAL ARG ALA GLU ILE MET ARG SER PHE SER LEU SER THR ASN LEU GLN GLU SER LEU ARG SER LYS GLU 160	AICITTICTI SER PHE SER L 150	TGİCAACAAA Bu sir tir ası	CTTGCAAGAA	IGTTTAAGAA Er lej arg si .60	GTAAGGAATG Be lys glu 165	jada.
	140 CYS ALA TRP GLU VAL V	VAL ARG ALA Œ	160 AL ARG ALA QLU ILE MET ARG SER LEU SER 1EU SER THR ASN LIJU QLN QLU ARG LIJU ARG ARG LYS QLU	SER LEU SER L	EU SER THR ASP	ו ובט מבא מבח ו	NG LEU ARG A	166 RG LYS GLU	•
2н(1)	ŢĠŢĠĊĊŢĠĠĠŔĠĠŦŢĠŦĊŔĠŔŖĠĊŔĠŔŖŦĊŖŦĠŖĠĸŢĊŢŢŢŢŢŢŢŢŢŖŖĠŖŔĠŖŔĠŖĸĠĠŖĸĠĠĸĸŢŦŖĸĠŖĸĠĠĸĸĠĠĸĸŢĸĸĊĸŢ 420 430 430 440 450 460 80	GTCAGAGCAG/	AĄATCATGAGA 40	TCCCTCTCTT	TAŢCĄACĄĄĄ	CTTGCAAGAA	IGAŢTAAGGA	GGAAGGAATA o	ACAT
:									

CIGGICCAACAIGAAAACAATICTIATIGACTCAIACACCAGGICACGTTICAIGAATICTGICATITCAAAGACTCTCACCCTGCTA sio sio sio sio 2н(1)

CTGGTTCAACATGGAAATGATTTCATTGATTCGTATGCCAGCTCACCTTTTATGA--TCTGCCATTTCAAAGACTCATGTTTCTGCTA

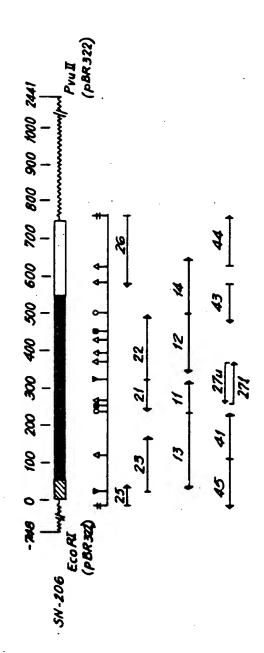
206(11)

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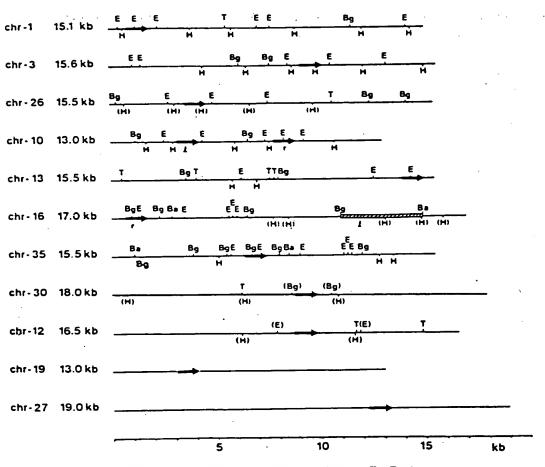
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206(11)	s90 IGACCATGACACGATTTA	610 AATCTTTCA	620 AAAİGTTT	630 TAGGÁGTA	640 TTAATCAAC	650 ATTGTATİCAG	660 CTCTTAÅGG	610 620 630 640 650 660 670 689 FAAATCTTTCAAATGTTTTTAGGAGTATTAATCAACATTGTATTCAGCTCTTAAGGCACTAGTCCCTTACAGAG	680 TACAGAĞ	•
2н(1)	TAACTATGACCATGCTGATATATTTAATATTTTATTTAACTATTCATAAGATTTAATTTTTTTGTTCATATAACGTC	TAAACTGATT 620	ITATCTATTT# 630	TAAATATI	TATTTAACT 640	ATTCATAAGA 650	TTAAATTA' 660	TTTTGTTCATA 670	TAACGTC 680	
206(11)	690 GACCATGCTĠAC ₂₉							· .		
2н(П)	ATGTGCACCTTTACACTGTGGTAGTGTAAAAACATGTTCCTTATATTTACTCAAAAAAC ₁₅ 690 700 710 720 730 740	TGGTTAGTG	IAATAAACA 720	ATGTTCC1	.TTATATTTAC 730	TCAAAAAAC 740	S			

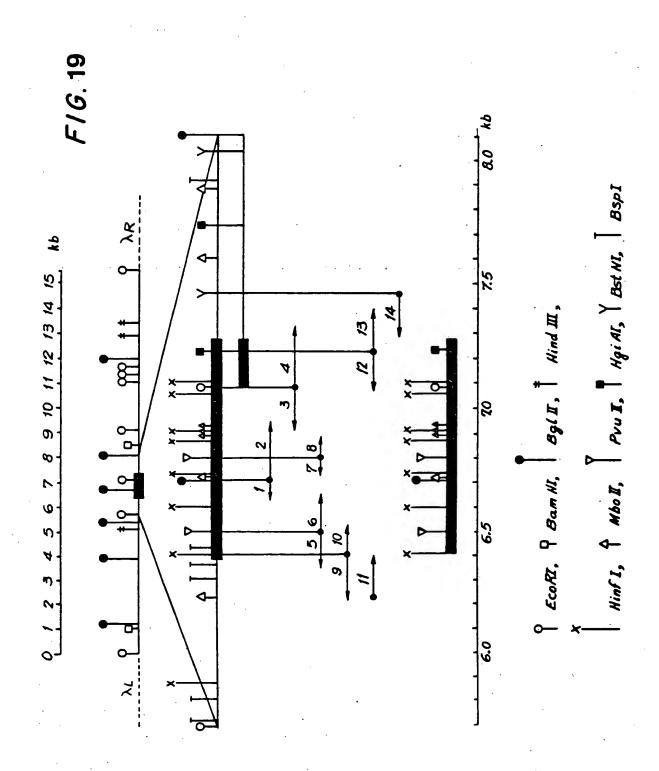
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PARTIAL RESTRICTION MAPS OF CLONED, IFN-→ RELATED CHROMOSOMAL DNA SEGMENTS



E: EcoRI, Ba: BamHI, Bg: BgIII, H: Hingil, T: Tacl



.0 6A	eu RI I	ευ 16 0R11
-140 GAAAGTGGCCCCAGAAGCATTAAGAAAGTGGAAATCAGTATGTTCCCTÄTTTAAGGCATTTGCAGGAAGCAAGGCCTTCAGAGAACCTÄGA Bsp1	S1 -40 -20 +1 metalaserprophealaleumetvalleu ICACCCATCTCAGCAAGCCCAGAAGTATCTGCAATATCTACGATGGCCTCGCCTTTGCTTTACTGATGGTCCTG BSPI AVAII	S20 1 10 100 100 100 100 100 100 100 100
CCTTCAG/	20 La leu leu TTTACTE	RGTHRLEU GGACCTTG AVAII S
-80 AAĠCAAGGCC BSPI	prophea CCCTTG	O 100 PASNARGAI TÅACAGGAU
TGCAGGA	talaser 66CCTC6 BSP I	10 TRLEUASP CCTGGATA ECORII
AAGGCATT	SJ +1 me ICTACGÅT	rhrhisse NCCACAG copi
-100 CCTÅTTI	TGCAATA	во <i>vprogluthrh</i> CCCTGAGACCC DDE I ECOP I
TATGTTC	-20 GÅAGTATC	YSASPLE GTGATCT MBOI
GAATCA(- AAGCCCAG] rleuglyc ICTGGGCT
-120 16AAAG†6(TCTCAGC	S20 60 60 6CTGCTC
AGCATTAA	-40 AGTCACCCA HINF	
-140 TGGCCCAGA/ BSPI	GCCCAAGGTTCAGAG1	40 valvalleuseroysl GTGGTGCTCAGCTGCA DDEI Pvull
-1 GAAAGTG B	GCCCAAG	vatvatteus GTGGTGCTCA DDE I

FIG. 20



20 140 ALAGLNNETSERARGILESERPROSERSERCYSLEUNETASPARGHISASPPHEGLYPHEPROGLNGLUGLUPHEASPGLYASNGLNPHE GCACAAATGAGCAGAATCTCCTCCTCCTCCTGTCGATGGACATGACTTTGGATTTCCCCCAGGAGGAGTTTGATGGCAACCAGTTC	50 220 220 240 240 260 260 260 280 280 300 300 CAGAAGCTCCACCATCTCCATGAGCTGATCCAGCAGATCTTTACCACAAAGATTCATCTGCTTGGGAT ALU MBO1/ Boli Mboi	80 320 340 340 350 360 360 360 360 360 360 360 360 360 36
30 160 161 ESERPROSERSERCYSLEUMETASPARGHISASPI 184 CTCCCTCCTCCTGTCTGÅTGGACAGACATGAC Hinf	60 260 210 SIESERVALLEUHISGLULEUILEGLNGLNILEPHEAS ATCTCTCCTCCATGAGCTGATCCAGCAGATCTTCAA ALU MBOI/ BGLII ECOP15 MBOI MBOII	320 340 340 SLYSPHECYSTHRGLULEUTYRGLNGLNLEUASNASP SAATTCTGCACCGAACTCTACCAGCAGCTGAATGAC ECOPIS PVUII
20 alagenwetserarg GCACAAATGAGCAGA H	50 220 GLMLYSALAPROALA CAGAAGĠCTCCAGCC	80 GLUASPLEULEUASP GAGGACCTCCTAGAC AVAII

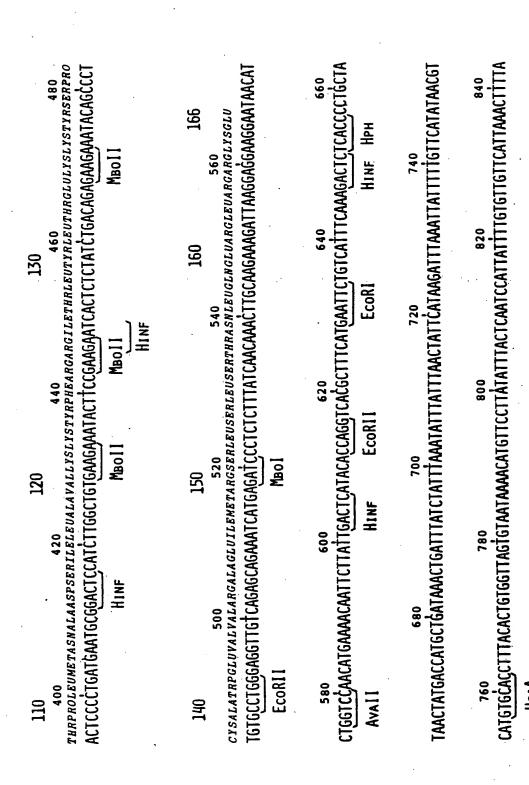
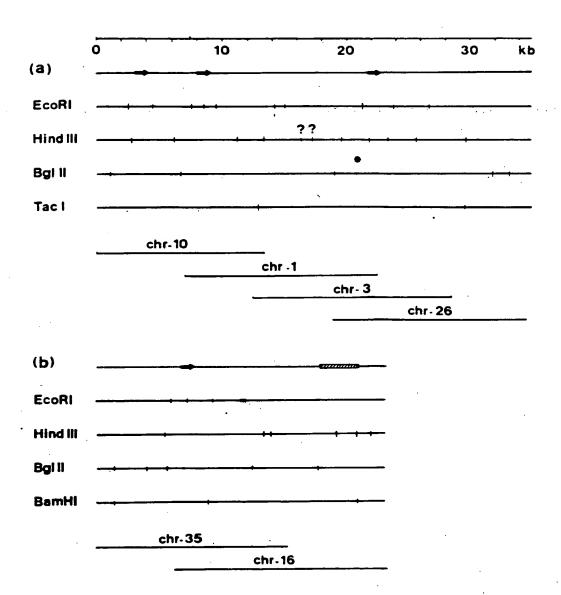


FIG. 22

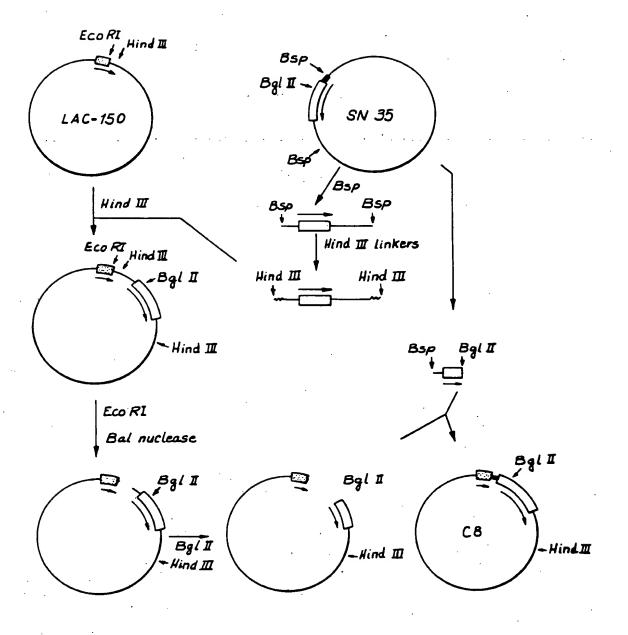
860 920 CTATAGGAACTTCCTGTAGTTCTTTAATATGAAATTCCTAGCCTGACTGTGCAACCTGATTAGAGAATAAAGGGTATATTTA

940 TTTGCTİATCATTATATATGTAAGA

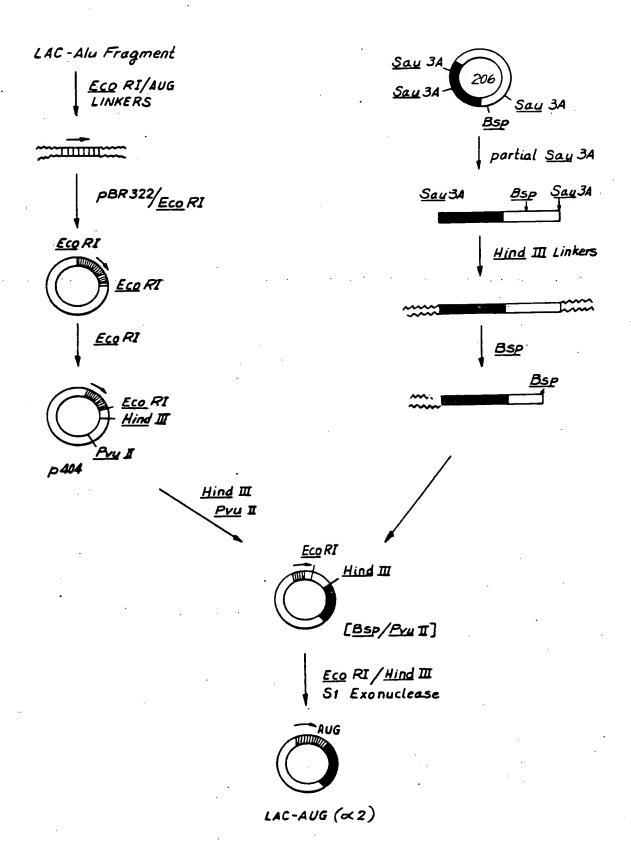
LINKAGE OF IFN- RELATED GENES



F1G. 25



F1G.26

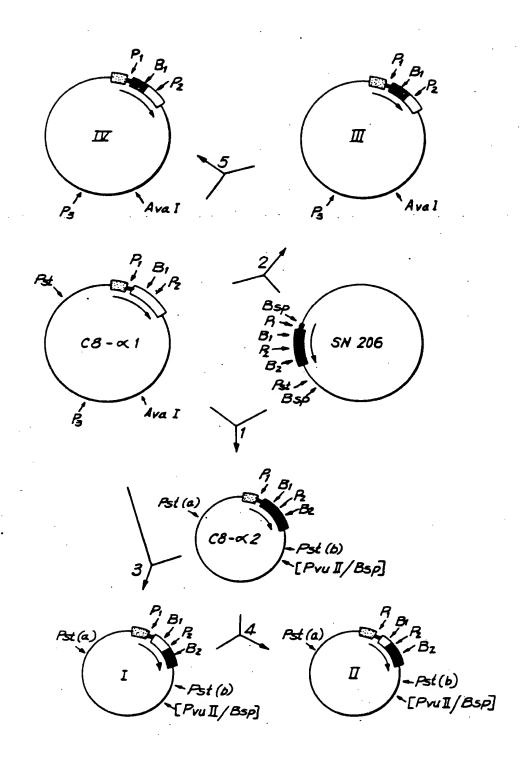


F1G.27

CONSTRUCTION OF PLASMID LAC-AUG (~-2)

IFN-& CDNA LAC PROMOTER LEUGLY CYS ASP CTGGGCTGTGAT . . ACAGICTATG . . . GACCCGACACTA''' ...TGTC GATAC''' SAU 3A ALUI ECO LINKER ...AAACAG _ CTATGAATTCATAG ACA AGETTGT + GAT ITTCTC GATACTTAAGTATC CTA TGTTCGAACA LIGASE LIGASE CYS ASP ACALAGETTGTGAT ... ACAGCTATE AATT CATAG ... TETCGATACTTAA GTATC HIND III Eco RI S1 NUCLEASE S 1 NUCLEASE ... ACAGCTATG TGTGAT TCTCGATAC * ACACTA ...

TGTCGATACACACTA



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200 TTATTTCTAGTAAA	300 TTACAAATTATTTT	400 ATTGGATATGTAAT	500 AAAGTTATTCCACA	600 GAATAAAAAGAGCA
$\begin{array}{cccccccccccccccccccccccccccccccccccc$	280 IACTGCAGCTGATGAAGT PSTI ALUI FYUII	380 ITTTAGGAGTTTTGAATG	480 ACATGAACAAATTACACT	580 STCATTCTTACTTACTTT
160 C ₂₄ AATGCAAA	260 ITGGCAACATCTGGATGAA	340 380 400 IJCATACACTAAGAGAAAAATTITAAAAAATTATTCATTCATATTTTTAGGAGTTTTGAATGATTGGATATGTAAT DDE I ECORI	480 500 CTATATAGATTITTATTTTGCATATGTACTTTGATACAAAATTTACATGAACAAATTACACTAAAGTTATTCCACA ECORI	540 560 600 STCAATAGCTTTTAAACTTAAATTTTAGTTTAGTTTAGTT
	240 GCTGAAAGAAAAAGTG1	340 ACTAAGAGAAAATTTTA/ DDEI ECORI	440 AGATTITTATTTTGCATATE ECORI	540 AGCTTTTAAACTTAAATTTT
	220 240 300 GITATICAACATCAGTACTTATGTCAACTGCTGAAAAAAAAAA	320 GTCATATAAAGCAAAATTCAAAGCTJCATAC EcoRI BBRI ALUI	420 TATATTCATATTATGTGTATCTATATA	520 ATATACTTATCAAATTAAGTTAATGTCAATA A

_		_		_	(21	Acui	o &
700	AATTA	800	GAAG	900	ICCTA(1000 116use CTCAG DDE I	ALLESER GAATCTCT I ECORI HHAII
	ATTIC 11		CGTAA		GAAAA	euva 1 1661(1000 SUILELEULEUGLNGLNMETGLYARGILESER IGATACICCTGCAACAATGGGAAGAATCTCT MBOIL ECORI
	GAAGAT		3AGT6		TCTTCA MBo I I	ggr <u>6</u> ggr66 l	<i>мете</i> АТGGG Мв
	ITCA		GTGA(IAAGT(VTGGCC BSPI	4ACAA
089	AAAAT	780	CACAT	880	GAGC#	980 <i>u1eu</i> ACTG	1080 1125061 1166(
•	ITATT		ITAAA		GCACA	8 <i>er1e</i> [CTT]	LELEU TACTO
	.TG16]		CTTT.		SCIATION IN	SCIII	
	AAATC	• •	MAAA	•	AAGACC	7. CT618	GAGGACC MNLI Asul
099	ATGCC	160	AAATG	860	TATTI	960 ITGGCC Asul BsP I	.060 TAGG/
	TAGAT		AAAAA		TTCAC	TCCAÄ	
	ATAAA.		IGATG.		GTATG	CAACA	GCCTGG BSTNI
	TATAC		GCAA		VATTA	ATTTĞ	CCACA
640	AGTAGAGGTATACGTAATATACATAAATAGATATGCCAAATCTGTGTTATTAAAATTTCATGAAGATTTCAATTA MALI MALI MBOII	740	MATA(840	IGGAATTTAGAAAATGGAAATTAGTATGTTCACTATTTAAGACCTATGCACAGAGCAAAGTCTTCAGAAAACCTAG ECORI	940 GCAAT/	1040 CTGTGATCTCAGACCCACAGCCTGGGTAATAGGAGGACCT DPN MNLI BSTNI MNLI MBOI DDEI
•	,TATA(16AM	w	GAAA	CCCAG	MNLI DDE I
	AGAGG Mal I		GCAGGTG HPHI		GAATTTA	AGTAG	GATCI GATCI DPN MBOI
	GAAGT		16A6T		AGGGA Ec	TCTCA	19175 19175
620	ICTGT.	720	36CTT	820	JAACT.	920 TATCCA	20 17 6 4 8 1 CTGG
9	TATCI	7;	AAAA(86	AGTAC RSA I	5.6 VLL 1091	1020 GTTCTC
	LTTT0		ACCAT		TAGAA	TTCA	ÇATCÎ
•	AACTTTGTAGTTTTTATCTCTGTGA		GAAAAAAATACCATAAAAGGCTTTGAGTGCAGGTGAAAATAGGCAATGATGAAAAAAATGAAAAACTTTTTAAACACATGTGAGAGTGCGTAAGAAGC Hphi		AAACAGAGATAGAAAGTACAACTAG RSAI	950 960 10000 AGGCCGAAGTTCAAGTTATCCATCTCAAGTAGCCCAGCAATATTTGCAACATCCAATGGCCCTGTCCTTTTCTTTACTGATGGCCGTGCTGATGGTGAGTGA	1020 tyrlysserilecysserleugli CJACAAATCCATCTGTTGTTCTGGGG UI ECORI
	AACT		GAAA		AAAC	AGGCCG MNLI BSPI	CTACAAATC
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FIG. 30

FIG. 31

1700	AGTTCTTTA	1800 TACCTTTAC	Rsal	
1680	ITGGTGTATACCGTGCAGGTACT RSAI	1780 1780 1780 1780 1780 1780 1780 1780 1780	. 02	
1660	GTTTTCAGCAGTGTGAAGAAGCT MBOLI BERI ALUI	1760 TATTTGTTTTAAAATTJAAAT	EcoRI	
1640	AGTTGAATCAAAATTTTCAAAT HAAII ECORI	1740 STCATCTATTTATTTGAATATT	1840	GTTCTTCATATTTAGCCAATA MB0111
1620	AAGACTCACTTCATAACCACCACGAGTTGAATCTTTTCAAATGTTTTCAGCAGTGTGGAAGGTTGGTGTATACCGTGCAGGTACTAGTTCTTTA HHAII BRI ALUI	1720 CAGATGACAATGCTGATGTCTCTGT1	1820	ATTGTGGTGGATGTAACGATATATGT

FIG 32